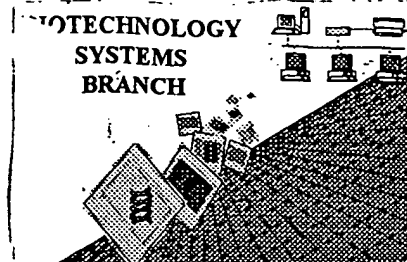


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1684

CRF Problem Report

The Scientific and Technical Information Center (STIC) experienced a problem when processing the following computer readable form (CRF):

Application Serial Number: 09/634,287
Filing Date: 8/9/2000
Date Processed by STIC: 3/4/2002

STIC Contact: Mark Spencer, 703-308-4212

Nature of Problem:

The CRF (was):

- ☒ (circle one) Damaged or Unreadable (for Unreadable, see attached)
☐ Blank (no files on CRF) (see attached)
☐ Empty file (filename present, but no bytes in file) (see attached)
☐ Virus-infected. Virus name: _____ The STIC will not process the CRF.
☐ Not saved in ASCII text
☐ Sequence Listing was embedded in the file. According to Sequence Rules, submitted file should **only** be the Sequence Listing.
☐ Did not contain a Sequence Listing. (see attached sample)
☐ Other: _____

**PLEASE USE THE CHECKER VERSION 3.1 PROGRAM TO REDUCE ERRORS.
SEE BELOW FOR ADDRESS:**

<http://www.uspto.gov/web/offices/pac/checker>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
3. Hand Carry directly to:
U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202
Or
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 01/29/2002

BEST AVAILABLE COPY

ADMP-1 Sequences

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS

- (A) LENGTH: 4192 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURES:

- (A) NAME/KEY: CDS
- (B) LOCATION: 406..2919

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

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AAG GCA CAG CGG AAG AAG GCA GAG ACA GGG CAG GCA CAG AAG CGG CCC	96
AGA CAG AGT CCT ACA GAG GGA GAG GCC AGA GAA GCT GCA GAA GAC ACA	144
GGC AGG GAG AGA CAA AGA TCC AGG AAA GGA GGG CTC AGG AGG AGA GTT	192
TGG AGA AGC CAG ACC CCT GGG CAC CTC TCC CAA GCC CAA GGA CTA AGT	240
TTT CTC CAT TTC CTT TAA CGG TCC TCA GCC CTT CTG AAA ACT TTG CCT	288
CTG ACC TTG GCA GGA GTC CAA GCC CCC AGG CTA CAG AGA GGA GCT TTC	336
CAA AGC TAG GGT GTG GAG GAC TTG GTG CCC TAG ACG GCC TCA GTC CCT	384
CCC AGC TGC AGT ACC AGT GCC ATG TCC CAG ACA GGC TCG CAT CCC GGG	432
Met Ser Gln Thr Gly Ser His Pro Gly	
AGG GGC TTG GCA GGG CGC TGG CTG TGG GGA GCC CAA CCC TGC CTC CTG	480
Arg Gly Leu Ala Gly Arg Trp Leu Trp Gly Ala Gln Pro Cys Leu Leu	
CTC CCC ATT GTG CCG CTC TCC TGG CTG GTG TGG CTG CTT CTG CTA CTG	528
Leu Pro Ile Val Pro Leu Ser Trp Leu Val Trp Leu Leu Leu Leu Leu	
CTG GCC TCT CTC CTG CCC TCA GCC CGG CTG GCC AGC CCC CTC CCC CGG	576
Leu Ala Ser Leu Leu Pro Ser Ala Arg Leu Ala Ser Pro Leu Pro Arg	
GAG GAG GAG ATC GTG TTT CCA GAG AAG CTC AAC GGC AGC GTC CTG CCT	624
Glu Glu Glu Ile Val Phe Pro Glu Lys Leu Asn Gly Ser Val Leu Pro	
GGC TCG GGC GCC CCT GCC AGG CTG TTG TGC CGC TTG CAG GCC TTT GGG	672
Gly Ser Gly Ala Pro Ala Arg Leu Leu Cys Arg Leu Gln Ala Phe Gly	
GAG ACG CTG CTA CTA GAG CTG GAG CAG GAC TCC GGT GTG CAG GTC GAG	720
Glu Thr Leu Leu Leu Glu Leu Glu Gln Asp Ser Gly Val Gln Val Glu	
GGG CTG ACA GTG CAG TAC CTG GGC CAG GCG CCT GAG CTG CTG GGT GGA	768
Gly Leu Thr Val Gln Tyr Leu Gly Gln Ala Pro Glu Leu Leu Gly Gly	
GCA GAG CCT GGC ACC TAC CTG ACT GGC ACC ATC AAT GGA GAT CCG GAG	816
Ala Glu Pro Gly Thr Tyr Leu Thr Gly Thr Ile Asn Gly Asp Pro Glu	

TCG	GTG	GCA	TCT	CTG	CAC	TGG	GAT	GGG	GGA	GCC	CTG	TTA	GGC	GTG	TTA	864
Ser	Val	Ala	Ser	Leu	His	Trp	Asp	Gly	Gly	Ala	Leu	Leu	Gly	Val	Leu	
CAA	TAT	CGG	GGG	GCT	GAA	CTC	CAC	CTC	CAG	CCC	CTG	GAG	GGA	GGC	ACC	912
Gln	Tyr	Arg	Gly	Ala	Glu	Leu	His	Leu	Gln	Pro	Leu	Glu	Gly	Gly	Thr	
CCT	AAC	TCT	GCT	GGG	GGA	CCT	GGG	GCT	CAC	ATC	CTA	CGC	CGG	AAG	AGT	960
Pro	Asn	Ser	Ala	Gly	Gly	Pro	Gly	Ala	His	Ile	Leu	Arg	Arg	Lys	Ser	
CCT	GCC	AGC	GGT	CAA	GGT	CCC	ATG	TGC	AAC	GTC	AAG	GCT	CCT	CTT	GGA	1008
Pro	Ala	Ser	Gly	Gln	Gly	Pro	Met	Cys	Asn	Val	Lys	Ala	Pro	Leu	Gly	
AGC	CCC	AGC	CCC	AGA	CCC	CGA	AGA	GCC	AAG	CGC	TTT	GCT	TCA	CTG	AGT	1056
Ser	Pro	Ser	Pro	Arg	Pro	Arg	Arg	Ala	Lys	Arg	Phe	Ala	Ser	Leu	Ser	
AGA	TTT	GTG	GAG	ACA	CTG	GTG	GTG	GCA	GAT	GAC	AAG	ATG	GCC	GCA	TTC	1104
Arg	Phe	Val	Glu	Thr	Leu	Val	Val	Ala	Asp	Asp	Lys	Met	Ala	Ala	Phe	
CAC	GGT	GCG	GGG	CTA	AAG	CGC	TAC	CTG	CTA	ACA	GTG	ATG	GCA	GCA	GCA	1152
His	Gly	Ala	Gly	Leu	Lys	Arg	Tyr	Leu	Leu	Thr	Val	Met	Ala	Ala	Ala	
GCC	AAG	GCC	TTC	AAG	CAC	CCA	AGC	ATC	CGC	AAT	CCT	GTC	AGC	TTG	GTG	1200
Ala	Lys	Ala	Phe	Lys	His	Pro	Ser	Ile	Arg	Asn	Pro	Val	Ser	Leu	Val	
GTG	ACT	CGG	CTA	GTG	ATC	CTG	GGG	TCA	GGC	GAG	GAG	GGG	CCC	CAA	GTG	1248
Val	Thr	Arg	Leu	Val	Ile	Leu	Gly	Ser	Gly	Glu	Glu	Gly	Pro	Gln	Val	
GGG	CCC	AGT	GCT	GCC	CAG	ACC	CTG	CGC	AGC	TTC	TGT	GCC	TGG	CAG	CGG	1296
Gly	Pro	Ser	Ala	Ala	Gln	Thr	Leu	Arg	Ser	Phe	Cys	Ala	Trp	Gln	Arg	
GGC	CTC	AAC	ACC	CCT	GAG	GAC	TCG	GAC	CCT	GAC	CAC	TTT	GAC	ACA	GCC	1344
Gly	Leu	Asn	Thr	Pro	Glu	Asp	Ser	Asp	Pro	Asp	His	Phe	Asp	Thr	Ala	
ATT	CTG	TTT	ACC	CGT	CAG	GAC	CTG	TGT	GGA	GTC	TCC	ACT	TGC	GAC	ACG	1392
Ile	Leu	Phe	Thr	Arg	Gln	Asp	Leu	Cys	Gly	Val	Ser	Thr	Cys	Asp	Thr	
CTG	GGT	ATG	GCT	GAT	GTG	GGC	ACC	GTC	TGT	GAC	CCG	GCT	CGG	AGC	TGT	1440
Leu	Gly	Met	Ala	Asp	Val	Gly	Thr	Val	Cys	Asp	Pro	Ala	Arg	Ser	Cys	
GCC	ATT	GTG	GAG	GAT	GAT	GGG	CTC	CAG	TCA	GCC	TTC	ACT	GCT	GCT	CAT	1488
Ala	Ile	Val	Glu	Asp	Asp	Gly	Leu	Gln	Ser	Ala	Phe	Thr	Ala	Ala	His	
GAA	CTG	GGT	CAT	GTC	TTC	AAC	ATG	CTC	CAT	GAC	AAC	TCC	AAG	CCA	TGC	1536
Glu	Leu	Gly	His	Val	Phe	Asn	Met	Leu	His	Asp	Asn	Ser	Lys	Pro	Cys	
ATC	AGT	TTG	AAT	GGG	CCT	TTG	AGC	ACC	TCT	CGC	CAT	GTC	ATG	GCC	CCT	1584
Ile	Ser	Leu	Asn	Gly	Pro	Leu	Ser	Thr	Ser	Arg	His	Val	Met	Ala	Pro	
GTG	ATG	GCT	CAT	GTG	GAT	CCT	GAG	GAG	CCC	TGG	TCC	CCC	TGC	AGT	GCC	1632
Val	Met	Ala	His	Val	Asp	Pro	Glu	Glu	Pro	Trp	Ser	Pro	Cys	Ser	Ala	
CGC	TTC	ATC	ACT	GAC	TTC	CTG	GAC	AAT	GGC	TAT	GGG	CAC	TGT	CTC	TTA	1680
Arg	Phe	Ile	Thr	Asp	Phe	Leu	Asp	Asn	Gly	Tyr	Gly	His	Cys	Leu	Leu	
GAC	AAA	CCA	GAG	GCT	CCA	TTG	CAT	CTG	CCT	GTG	ACT	TTC	CCT	GGC	AAG	1728
Asp	Lys	Pro	Glu	Ala	Pro	Leu	His	Leu	Pro	Val	Thr	Phe	Pro	Gly	Lys	
GAC	TAT	GAT	GCT	GAC	CGC	CAG	TGC	CAG	CTG	ACC	TTC	GGG	CCC	GAC	TCA	1776
Asp	Tyr	Asp	Ala	Asp	Arg	Gln	Cys	Gln	Leu	Thr	Phe	Gly	Pro	Asp	Ser	
CGC	CAT	TGT	CCA	CAG	CTG	CCG	CCG	CCC	TGT	GCT	GCC	CTC	TGG	TGC	TCT	1824
Arg	His	Cys	Pro	Gln	Leu	Pro	Pro	Pro	Cys	Ala	Ala	Leu	Trp	Cys	Ser	

GGC	CAC	CTC	AAT	GGC	CAT	GCC	ATG	TGC	CAG	ACC	AAA	CAC	TCG	CCC	TGG	1872
Gly	His	Leu	Asn	Gly	His	Ala	Met	Cys	Gln	Thr	Lys	His	Ser	Pro	Trp	
GCC	GAT	GGC	ACA	CCC	TGC	GGG	CCC	GCA	CAG	GCC	TGC	ATG	GGT	GGT	CGC	1920
Ala	Asp	Gly	Thr	Pro	Cys	Gly	Pro	Ala	Gln	Ala	Cys	Met	Gly	Gly	Arg	
TGC	CTC	CAC	ATG	GAC	CAG	CTC	CAG	GAC	TTC	AAT	ATT	CCA	CAG	GCT	GGT	1968
Cys	Leu	His	Met	Asp	Gln	Leu	Gln	Asp	Phe	Asn	Ile	Pro	Gln	Ala	Gly	
GGC	TGG	GGT	CCT	TGG	GGA	CCA	TGG	GGT	GAC	TGC	TCT	CGG	ACC	TGT	GGG	2016
Gly	Trp	Gly	Pro	Trp	Gly	Pro	Trp	Gly	Asp	Cys	Ser	Arg	Thr	Cys	Gly	
GGT	GGT	GTC	CAG	TTC	TCC	TCC	CGA	GAC	TGC	ACG	AGG	CCT	GTC	CCC	CGG	2064
Gly	Gly	Val	Gln	Phe	Ser	Ser	Arg	Asp	Cys	Thr	Arg	Pro	Val	Pro	Arg	
AAT	GGT	GGC	AAG	TAC	TGT	GAG	GGC	CGC	CGT	ACC	CGC	TTC	CGC	TCC	TGC	2112
Asn	Gly	Gly	Lys	Tyr	Cys	Glu	Gly	Arg	Arg	Thr	Arg	Phe	Arg	Ser	Cys	
AAC	ACT	GAG	GAC	TGC	CCA	ACT	GGC	TCA	GCC	CTG	ACC	TTC	CGC	GAG	GAG	2160
Asn	Thr	Glu	Asp	Cys	Pro	Thr	Gly	Ser	Ala	Leu	Thr	Phe	Arg	Glu	Glu	
CAG	TGT	GCT	GCC	TAC	AAC	CAC	CGC	ACC	GAC	CTC	TTC	AAG	AGC	TTC	CCA	2208
Gln	Cys	Ala	Ala	Tyr	Asn	His	Arg	Thr	Asp	Leu	Phe	Lys	Ser	Phe	Pro	
GGG	CCC	ATG	GAC	TGG	GTT	CCT	CGC	TAC	ACA	GGC	GTG	GCC	CCC	CAG	GAC	2256
Gly	Pro	Met	Asp	Trp	Val	Pro	Arg	Tyr	Thr	Gly	Val	Ala	Pro	Gln	Asp	
CAG	TGC	AAA	CTC	ACC	TGC	CAG	GCC	CGG	GCA	CTG	GGC	TAC	TAC	TAT	GTG	2304
Gln	Cys	Lys	Leu	Thr	Cys	Gln	Ala	Arg	Ala	Leu	Gly	Tyr	Tyr	Tyr	Val	
CTG	GAG	CCA	CGG	GTG	GTA	GAT	GGG	ACC	CCC	TGT	TCC	CCG	GAC	AGC	TCC	2352
Leu	Glu	Pro	Arg	Val	Val	Asp	Gly	Thr	Pro	Cys	Ser	Pro	Asp	Ser	Ser	
TCG	GTC	TGT	GTC	CAG	GGC	CGA	TGC	ATC	CAT	GCT	GGC	TGT	GAT	CGC	ATC	2400
Ser	Val	Cys	Val	Gln	Gly	Arg	Cys	Ile	His	Ala	Gly	Cys	Asp	Arg	Ile	
ATT	GGC	TCC	AAG	AAG	AAG	TTT	GAC	AAG	TGC	ATG	GTG	TGC	GGA	GGG	GAC	2448
Ile	Gly	Ser	Lys	Lys	Lys	Phe	Asp	Lys	Cys	Met	Val	Cys	Gly	Gly	Asp	
GGT	TCT	GGT	TGC	AGC	AAG	CAG	TCA	GGC	TCC	TTC	AGG	AAA	TTC	AGG	TAC	2496
Gly	Ser	Gly	Cys	Ser	Lys	Gln	Ser	Gly	Ser	Phe	Arg	Lys	Phe	Arg	Tyr	
GGA	TAC	AAC	AAT	GTG	GTC	ACT	ATC	CCC	GCG	GGG	GCC	ACC	CAC	ATT	CTT	2544
Gly	Tyr	Asn	Asn	Val	Val	Thr	Ile	Pro	Ala	Gly	Ala	Thr	His	Ile	Leu	
GTC	CGG	CAG	CAG	GGA	AAC	CCT	GGC	CAC	CGG	AGC	ATC	TAC	TTG	GCC	CTG	2592
Val	Arg	Gln	Gln	Gly	Asn	Pro	Gly	His	Arg	Ser	Ile	Tyr	Leu	Ala	Leu	
AAG	CTG	CCA	GAT	GGC	TCC	TAT	GCC	CTC	AAT	GGT	GAA	TAC	ACG	CTG	ATG	2640
Lys	Leu	Pro	Asp	Gly	Ser	Tyr	Ala	Leu	Asn	Gly	Glu	Tyr	Thr	Leu	Met	
CCC	TCC	CCC	ACA	GAT	GTG	GTA	CTG	CCT	GGG	GCA	GTC	AGC	TTG	CGC	TAC	2688
Pro	Ser	Pro	Thr	Asp	Val	Val	Leu	Pro	Gly	Ala	Val	Ser	Leu	Arg	Tyr	
AGC	GGG	GCC	ACT	GCA	GCC	TCA	GAG	ACA	CTG	TCA	GGC	CAT	GGG	CCA	CTG	2736
Ser	Gly	Ala	Thr	Ala	Ala	Ser	Glu	Thr	Leu	Ser	Gly	His	Gly	Pro	Leu	
GCC	CAG	CCT	TTG	ACA	CTG	CAA	GTC	CTA	GTG	GCT	GGC	AAC	CCC	CAG	GAC	2784
Ala	Gln	Pro	Leu	Thr	Leu	Gln	Val	Leu	Val	Ala	Gly	Asn	Pro	Gln	Asp	
ACA	CGC	CTC	CGA	TAC	AGC	TTC	TTC	GTG	CCC	CGG	CCG	ACC	CCT	TCA	ACG	2832
Thr	Arg	Leu	Arg	Tyr	Ser	Phe	Phe	Val	Pro	Arg	Pro	Thr	Pro	Ser	Thr	
CCA	CGC	CCC	ACT	CCC	CAG	GAC	TGG	CTG	CAC	CGA	AGA	GCA	CAG	ATT	CTG	2880

Pro	Arg	Pro	Thr	Pro	Gln	Asp	Trp	Leu	His	Arg	Arg	Ala	Gln	Ile	Leu		
GAG	ATC	CTT	CGG	CGG	CGC	CCC	TGG	GCG	GGC	AGG	AAA	TAA	CCT	CAC	TAT	2928	
Glu	Ile	Leu	Arg	Arg	Arg	Pro	Trp	Ala	Gly	Arg	Lys	End					
CCC	GGC	TGC	CCT	TTC	TGG	GCA	CCG	GGG	CCT	CGG	ACT	TAG	CTG	GGA	GAA	2976	
AGA	GAG	AGC	TTC	TGT	TGC	TGC	CTC	ATG	CTA	AGA	CTC	AGT	GGG	GAG	GGG	3024	
CTG	TGG	GCG	TGA	GAC	CTG	CCC	CTC	CTC	TCT	GCC	CTA	ATG	CGC	AGG	CTG	3072	
GCC	CTG	CCC	TGG	TTT	CCT	GCC	CTG	GGA	GGC	AGT	GAT	GGG	TTA	GTG	GAT	3120	
GGA	AGG	GGC	TGA	CAG	ACA	GCC	CTC	CAT	CTA	AAC	TGC	CCC	CTC	TGC	CCT	3168	
GCG	GGT	CAC	AGG	AGG	GAG	GGG	GAA	GGC	AGG	GAG	GGC	CTG	GGC	CCC	AGT	3216	
TGT	ATT	TAT	TTA	GTA	TTT	ATT	CAC	TTT	TAT	TTA	GCA	CCA	GGG	AAG	GGG	3264	
ACA	AGG	ACT	AGG	GTC	CTG	GGG	AAC	CTG	ACC	CCT	GAC	CCC	TCA	TAG	CCC	3312	
TCA	CCC	TGG	GGC	TAG	GAA	ATC	CAG	GGT	GGT	GGT	GAT	AGG	TAT	AAG	TGG	3360	
TGT	GTG	TAT	GCG	TGT	GTG	TGT	GTG	TGT	GAA	AAT	GTG	TGT	GTG	CTT	ATG	3408	
TAT	GAG	GTA	CAA	CCT	GTT	CTG	CTT	TCC	TCT	TCC	TGA	ATT	TTA	TTT	TTT	3456	
GGG	AAA	AGA	AAA	GTC	AAG	GGT	AGG	GTG	GGC	CTT	CAG	GGA	GTG	AGG	GAT	3504	
TAT	CCT	TTT	TTT	TTT	CTT	TCT	TTC	TTT	CTT	TTT	TTT	TTT	GAG	ACA	GAA	3552	
TCT	CGC	TCT	GTC	GCC	CAG	GCT	GGA	GTG	CAA	TGG	CAC	AAT	CTC	GGC	TCA	3600	
CTG	CAT	CCT	CCG	CCT	CCC	GGG	TTC	AAG	TGA	TTC	TCA	TGC	CTC	AGC	CTC	3648	
CTG	AGT	AGC	TGG	GAT	TAC	AGG	CTC	CTG	CCA	CCA	CGC	CCG	GCT	AAT	TTT	3696	
TGT	TTT	GTT	TTG	TTT	GGA	GAC	AGA	GTC	TCG	CTA	TTG	TCA	CCA	GGG	CTG	3744	
GAA	TGA	TTT	CAG	CTC	ACT	GCA	ACC	TTC	GCC	ACC	TGG	GTT	CCA	GCA	ATT	3792	
CTC	CTG	CCT	CAG	CCT	CCC	GAG	TAG	CTG	AGA	TTA	TAG	GCA	CCT	ACC	ACC	3840	
ACG	CCC	GGC	TAA	TTT	TTG	TAT	TTT	TAG	TAG	AGA	CGG	GGT	TTC	ACC	ATG	3888	
TTG	GCC	AGG	CTG	GTC	TCG	AAC	TCC	TGA	CCT	TAG	GTG	ATC	CAC	TCG	CCT	3936	
TCA	TCT	CCC	AAA	GTG	CTG	GGA	TTA	CAG	GCG	TGA	GCC	ACC	GTG	CCT	GGC	3984	
CAC	GCC	CAA	CTA	ATT	TTT	GTA	TTT	TTA	GTA	GAG	ACA	GGG	TTT	CAC	CAT	4032	
GTT	GGC	CAG	GCT	GCT	CTT	GAA	CTC	CTG	ACC	TCA	GGT	AAT	CGA	CCT	GCC	4080	
TCG	GCC	TCC	CAA	AGT	GCT	GGG	ATT	ACA	GGT	GTG	AGC	CAC	CAC	GCC	CGG	4128	
TAC	ATA	TTT	TTT	AAA	TTG	AAT	TCT	ACT	ATT	TAT	GTG	ATC	CTT	TTG	GAG	4176	
TCA	GAC	AGA	TGT	GGG	T											4192	

(2) INFORMATION FOR SEQ ID NO:2:
 (i) SEQUENCE CHARACTERISTICS

(A) LENGTH: 837 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Ser Gln Thr Gly Ser His Pro Gly Arg Gly Leu Ala Gly Arg Trp	16
Leu Trp Gly Ala Gln Pro Cys Leu Leu Leu Pro Ile Val Pro Leu Ser	32
Trp Leu Val Trp Leu Leu Leu Leu Leu Leu Ala Ser Leu Leu Pro Ser	48
Ala Arg Leu Ala Ser Pro Leu Pro Arg Glu Glu Glu Ile Val Phe Pro	64
Glu Lys Leu Asn Gly Ser Val Leu Pro Gly Ser Gly Ala Pro Ala Arg	80
Leu Leu Cys Arg Leu Gln Ala Phe Gly Glu Thr Leu Leu Leu Glu Leu	96
Glu Gln Asp Ser Gly Val Gln Val Glu Gly Leu Thr Val Gln Tyr Leu	112
Gly Gln Ala Pro Glu Leu Leu Gly Gly Ala Glu Pro Gly Thr Tyr Leu	128
Thr Gly Thr Ile Asn Gly Asp Pro Glu Ser Val Ala Ser Leu His Trp	144
Asp Gly Gly Ala Leu Leu Gly Val Leu Gln Tyr Arg Gly Ala Glu Leu	160
His Leu Gln Pro Leu Glu Gly Gly Thr Pro Asn Ser Ala Gly Gly Pro	176
Gly Ala His Ile Leu Arg Arg Lys Ser Pro Ala Ser Gly Gln Gly Pro	192
Met Cys Asn Val Lys Ala Pro Leu Gly Ser Pro Ser Pro Arg Pro Arg	208
Arg Ala Lys Arg Phe Ala Ser Leu Ser Arg Phe Val Glu Thr Leu Val	224
Val Ala Asp Asp Lys Met Ala Ala Phe His Gly Ala Gly Leu Lys Arg	240
Tyr Leu Leu Thr Val Met Ala Ala Ala Ala Lys Ala Phe Lys His Pro	256
Ser Ile Arg Asn Pro Val Ser Leu Val Val Thr Arg Leu Val Ile Leu	272
Gly Ser Gly Glu Glu Gly Pro Gln Val Gly Pro Ser Ala Ala Gln Thr	288
Leu Arg Ser Phe Cys Ala Trp Gln Arg Gly Leu Asn Thr Pro Glu Asp	304
Ser Asp Pro Asp His Phe Asp Thr Ala Ile Leu Phe Thr Arg Gln Asp	320
Leu Cys Gly Val Ser Thr Cys Asp Thr Leu Gly Met Ala Asp Val Gly	336
Thr Val Cys Asp Pro Ala Arg Ser Cys Ala Ile Val Glu Asp Asp Gly	352
Leu Gln Ser Ala Phe Thr Ala Ala His Glu Leu Gly His Val Phe Asn	368
Met Leu His Asp Asn Ser Lys Pro Cys Ile Ser Leu Asn Gly Pro Leu	384
Ser Thr Ser Arg His Val Met Ala Pro Val Met Ala His Val Asp Pro	400
Glu Glu Pro Trp Ser Pro Cys Ser Ala Arg Phe Ile Thr Asp Phe Leu	416
Asp Asn Gly Tyr Gly His Cys Leu Leu Asp Lys Pro Glu Ala Pro Leu	432
His Leu Pro Val Thr Phe Pro Gly Lys Asp Tyr Asp Ala Asp Arg Gln	448

Cys	Gln	Leu	Thr	Phe	Gly	Pro	Asp	Ser	Arg	His	Cys	Pro	Gln	Leu	Pro	464
Pro	Pro	Cys	Ala	Ala	Leu	Trp	Cys	Ser	Gly	His	Leu	Asn	Gly	His	Ala	480
Met	Cys	Gln	Thr	Lys	His	Ser	Pro	Trp	Ala	Asp	Gly	Thr	Pro	Cys	Gly	496
Pro	Ala	Gln	Ala	Cys	Met	Gly	Gly	Arg	Cys	Leu	His	Met	Asp	Gln	Leu	512
Gln	Asp	Phe	Asn	Ile	Pro	Gln	Ala	Gly	Gly	Trp	Gly	Pro	Trp	Gly	Pro	528
Trp	Gly	Asp	Cys	Ser	Arg	Thr	Cys	Gly	Gly	Gly	Val	Gln	Phe	Ser	Ser	544
Arg	Asp	Cys	Thr	Arg	Pro	Val	Pro	Arg	Asn	Gly	Gly	Lys	Tyr	Cys	Glu	560
Gly	Arg	Arg	Thr	Arg	Phe	Arg	Ser	Cys	Asn	Thr	Glu	Asp	Cys	Pro	Thr	576
Gly	Ser	Ala	Leu	Thr	Phe	Arg	Glu	Glu	Gln	Cys	Ala	Ala	Tyr	Asn	His	592
Arg	Thr	Asp	Leu	Phe	Lys	Ser	Phe	Pro	Gly	Pro	Met	Asp	Trp	Val	Pro	608
Arg	Tyr	Thr	Gly	Val	Ala	Pro	Gln	Asp	Gln	Cys	Lys	Leu	Thr	Cys	Gln	624
Ala	Arg	Ala	Leu	Gly	Tyr	Tyr	Tyr	Val	Leu	Glu	Pro	Arg	Val	Val	Asp	640
Gly	Thr	Pro	Cys	Ser	Pro	Asp	Ser	Ser	Ser	Val	Cys	Val	Gln	Gly	Arg	656
Cys	Ile	His	Ala	Gly	Cys	Asp	Arg	Ile	Ile	Gly	Ser	Lys	Lys	Lys	Phe	672
Asp	Lys	Cys	Met	Val	Cys	Gly	Gly	Asp	Gly	Ser	Gly	Cys	Ser	Lys	Gln	688
Ser	Gly	Ser	Phe	Arg	Lys	Phe	Arg	Tyr	Gly	Tyr	Asn	Asn	Val	Val	Thr	704
Ile	Pro	Ala	Gly	Ala	Thr	His	Ile	Leu	Val	Arg	Gln	Gln	Gly	Asn	Pro	720
Gly	His	Arg	Ser	Ile	Tyr	Leu	Ala	Leu	Lys	Leu	Pro	Asp	Gly	Ser	Tyr	736
Ala	Leu	Asn	Gly	Glu	Tyr	Thr	Leu	Met	Pro	Ser	Pro	Thr	Asp	Val	Val	752
Leu	Pro	Gly	Ala	Val	Ser	Leu	Arg	Tyr	Ser	Gly	Ala	Thr	Ala	Ala	Ser	768
Glu	Thr	Leu	Ser	Gly	His	Gly	Pro	Leu	Ala	Gln	Pro	Leu	Thr	Leu	Gln	784
Val	Leu	Val	Ala	Gly	Asn	Pro	Gln	Asp	Thr	Arg	Leu	Arg	Tyr	Ser	Phe	800
Phe	Val	Pro	Arg	Pro	Thr	Pro	Ser	Thr	Pro	Arg	Pro	Thr	Pro	Gln	Asp	816
Trp	Leu	His	Arg	Arg	Ala	Gln	Ile	Leu	Glu	Ile	Leu	Arg	Arg	Arg	Pro	832
Trp	Ala	Gly	Arg	Lys												837

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS

- (A) LENGTH: 27 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

FASLSRVETLVVADDKMAAFHGAGLK

(2) INFORMATION FOR SEQ ID NO:5:
 (i) SEQUENCE CHARACTERISTICS
 (A) LENGTH: 7 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

 (ii) MOECULE TYPE: peptide

 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:
YTGVA PR

(2) INFORMATION FOR SEQ ID NO:6:
 (i) SEQUENCE CHARACTERISTICS
 (A) LENGTH: 27 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

 (ii) MOECULE TYPE: peptide

 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:
ALGYYYVLDPR

(2) INFORMATION FOR SEQ ID NO:7:
 (i) SEQUENCE CHARACTERISTICS
 (A) LENGTH: 21 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

 (iii) HYPOTHETICAL: NO

 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:
GGGGGTGGTGTCCAGTTCTCC

(2) INFORMATION FOR SEQ ID NO:8:
 (i) SEQUENCE CHARACTERISTICS
 (A) LENGTH: 23 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

 (iii) HYPOTHETICAL: NO

 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:
GGCCCTGGAAAGCTCTGAAGAG

(2) INFORMATION FOR SEQ ID NO:9:
 (i) SEQUENCE CHARACTERISTICS
 (A) LENGTH: 23 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

 (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CCCCGGAATGGTGGCAAGTACTG

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

ACCCACATCTGTCTGACTCCAAA

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

CCAGTTGGGCAGTCCTCAGTGTT

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GGTCGGTGCGGTGGTTGTAGGC

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS

- (A) LENGTH: 17 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CASLSRFVETLVVADDK

ADMP-2 Sequences

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS

- (A) LENGTH: 3250 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURES:

- (A) NAME/KEY: CDS
- (B) LOCATION: 121..2913

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

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TGA CTC AAT CCT GCA AGC AAG TGT GTG TGT GTC CCC ATC CCC CGC CCC 48
GTT AAC TTC ATA GCA AAT AAC AAA TAC CCA TAA AGT CCC AGT CGC GCA 96
GCC CCT CCC CGC GGG CAG CGC ACT ATG CTG CTC GGG TGG GCG TCC CTG 144
Met Leu Leu Gly Trp Ala Ser Leu
CTG CTG TGC GCG TTC CGC CTG CCC CTG GCC GCG GTC GGC CCC GCC GCG 192
Leu Leu Cys Ala Phe Arg Leu Pro Leu Ala Ala Val Gly Pro Ala Ala
ACA CCT GCC CAG GAT AAA GCC GGG CAG CCT CCG ACT GCT GCA GCA GCC 240
Thr Pro Ala Gln Asp Lys Ala Gly Gln Pro Pro Thr Ala Ala Ala Ala
GCC CAG CCC CGC CGG CGG CAG GGG GAG GAG GTG CAG GAG CGA GCC GAG 288
Ala Gln Pro Arg Arg Arg Gln Gly Glu Glu Val Gln Glu Arg Ala Glu
CCT CCC GGC CAC CCG CAC CCC CTG GCG CAG CGG CGC AGG AGC AAG GGG 336
Pro Pro Gly His Pro His Pro Leu Ala Gln Arg Arg Arg Ser Lys Gly
CTG GTG CAG AAC ATC GAC CAA CTC TAC TCC GGC GGC GGC AAG GTG GGC 384
Leu Val Gln Asn Ile Asp Gln Leu Tyr Ser Gly Gly Gly Lys Val Gly
TAC CTC GTC TAC GCG GGC GGC CGG AGG TTC CTC TTG GAC CTG GAG CGA 432
Tyr Leu Val Tyr Ala Gly Gly Arg Arg Phe Leu Leu Asp Leu Glu Arg
GAT GGT TCG GTG GGC ATT GCT GGC TTC GTG CCC GCA GGA GGC GGG ACG 480
Asp Gly Ser Val Gly Ile Ala Gly Phe Val Pro Ala Gly Gly Gly Thr
AGT GCG CCC TGG CGC CAC CGG AGC CAC TGC TTC TAT CGG GGC ACA GTG 528
Ser Ala Pro Trp Arg His Arg Ser His Cys Phe Tyr Arg Gly Thr Val
GAC GCT AGT CCC CGC TCT CTG GCT GTC TTT GAC CTC TGT GGG GGT CTC 576
Asp Ala Ser Pro Arg Ser Leu Ala Val Phe Asp Leu Cys Gly Gly Leu
GAC GGC TTC TTC GCG GTC AAG CAC GCG CGC TAC ACC CTA AAG CCA CTG 624
Asp Gly Phe Phe Ala Val Lys His Ala Arg Tyr Thr Leu Lys Pro Leu
CTG CGC GGA CCC TGG GCG GAG GAA GAA AAG GGG CGC GTG TAC GGG GAT 672
Leu Arg Gly Pro Trp Ala Glu Glu Glu Lys Gly Arg Val Tyr Gly Asp
GGG TCC GCA CGG ATC CTG CAC GTC TAC ACC CGC GAG GGC TTC AGC TTC 720
Gly Ser Ala Arg Ile Leu His Val Tyr Thr Arg Glu Gly Phe Ser Phe

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GAG GCC CTG CCG CCG CGC GCC AGC TGC GAA ACC CCC GCG TCC ACA CCG 768
 Glu Ala Leu Pro Pro Arg Ala Ser Cys Glu Thr Pro Ala Ser Thr Pro
 GAG GCC CAC GAG CAT GCT CCG GCG CAC AGC AAC CCG AGC GGA CGC GCA 816
 Glu Ala His Glu His Ala Pro Ala His Ser Asn Pro Ser Gly Arg Ala
 GCA CTG GCC TCG CAG CTC TTG GAC CAG TCC GCT CTC TCG CCC GCT GGG 864
 Ala Leu Ala Ser Gln Leu Leu Asp Gln Ser Ala Leu Ser Pro Ala Gly
 GGC TCA GGA CCG CAG ACG TGG TGG CGG CGG CGG CGC CGC TCC ATC TCC 912
 Gly Ser Gly Pro Gln Thr Trp Trp Arg Arg Arg Arg Arg Ser Ile Ser
 CGG GCC CGC CAG GTG GAG CTG CTT CTG GTG GCT GAC GCG TCC ATG GCG 960
 Arg Ala Arg Gln Val Glu Leu Leu Leu Val Ala Asp Ala Ser Met Ala
 CGG TTG TAT GGC CGG GGC CTG CAG CAT TAC CTG CTG ACC CTG GCC TCC 1008
 Arg Leu Tyr Gly Arg Gly Leu Gln His Tyr Leu Leu Thr Leu Ala Ser
 ATC GCC AAT AGG CTG TAC AGC CAT GCT AGC ATC GAG AAC CAC ATC CGC 1056
 Ile Ala Asn Arg Leu Tyr Ser His Ala Ser Ile Glu Asn His Ile Arg
 CTG GCC GTG GTG AAG GTG GTG GTG CTA GGC GAC AAG GAC AAG AGC CTG 1104
 Leu Ala Val Val Lys Val Val Val Leu Gly Asp Lys Asp Lys Ser Leu
 GAA GTG AGC AAG AAC GCT GCC ACC ACA CTC AAG AAC TTT TGC AAG TGG 1152
 Glu Val Ser Lys Asn Ala Ala Thr Thr Leu Lys Asn Phe Cys Lys Trp
 CAG CAC CAA CAC AAC CAG CTG GGA GAT GAC CAT GAG GAG CAC TAC GAT 1200
 Gln His Gln His Asn Gln Leu Gly Asp Asp His Glu Glu His Tyr Asp
 GCA GCT ATC CTG TTT ACT CGG GAG GAT TTA TGT GGG CAT CAT TCA TGT 1248
 Ala Ala Ile Leu Phe Thr Arg Glu Asp Leu Cys Gly His His Ser Cys
 GAC ACC CTG GGA ATG GCA GAC GTT GGG ACC ATA TGT TCT CCA GAG CGC 1296
 Asp Thr Leu Gly Met Ala Asp Val Gly Thr Ile Cys Ser Pro Glu Arg
 AGC TGT GCT GTG ATT GAA GAC GAT GGC CTC CAC GCA GCC TTC ACT GTG 1344
 Ser Cys Ala Val Ile Glu Asp Asp Gly Leu His Ala Ala Phe Thr Val
 GCT CAC GAA ATC GGA CAT TTA CTT GGC CTC TCC CAT GAC GAT TCC AAA 1392
 Ala His Glu Ile Gly His Leu Leu Gly Leu Ser His Asp Asp Ser Lys
 TTC TGT GAA GAG ACC TTT GGT TCC ACA GAA GAT AAG CGC TTA ATG TCT 1440
 Phe Cys Glu Glu Thr Phe Gly Ser Thr Glu Asp Lys Arg Leu Met Ser
 TCC ATC CTT ACC AGC ATT GAT GCA TCT AAG CCC TGG TCC AAA TGC ACT 1488
 Ser Ile Leu Thr Ser Ile Asp Ala Ser Lys Pro Trp Ser Lys Cys Thr
 TCA GCC ACC ATC ACA GAA TTC CTG GAT GAT GGC CAT GGT AAC TGT TTG 1536
 Ser Ala Thr Ile Thr Glu Phe Leu Asp Asp Gly His Gly Asn Cys Leu
 CTG GAC CTA CCA CGA AAG CAG ATC CTG GGC CCC GAA GAA CTC CCA GGA 1584
 Leu Asp Leu Pro Arg Lys Gln Ile Leu Gly Pro Glu Glu Leu Pro Gly
 CAG ACC TAC GAT GCC ACC CAG CAG TGC AAC CTG ACA TTC GGG CCT GAG 1632
 Gln Thr Tyr Asp Ala Thr Gln Gln Cys Asn Leu Thr Phe Gly Pro Glu
 TAC TCC GTG TGT CCC GGC ATG GAT GTC TGT GCT CGC CTG TGG TGT GCT 1680
 Tyr Ser Val Cys Pro Gly Met Asp Val Cys Ala Arg Leu Trp Cys Ala
 GTG GTA CGC CAG GGC CAG ATG GTC TGT CTG ACC AAG AAG CTG CCT GCG 1728
 Val Val Arg Gln Gly Gln Met Val Cys Leu Thr Lys Lys Leu Pro Ala

GTG GAA GGG ACG CCT TGT GGA AAG GGG AGA ATC TGC CTG CAG GGC AAA 1776
 Val Glu Gly Thr Pro Cys Gly Lys Gly Arg Ile Cys Leu Gln Gly Lys
 TGT GTG GAC AAA ACC AAG AAA AAA TAT TAT TCA ACG TCA AGC CAT GGC 1824
 Cys Val Asp Lys Thr Lys Lys Lys Tyr Tyr Ser Thr Ser Ser His Gly
 AAC TGG GGA TCT TGG GGA TCC TGG GGC CAG TGT TCT CGC TCA TGT GGA 1872
 Asn Trp Gly Ser Trp Gly Ser Trp Gly Gln Cys Ser Arg Ser Cys Gly
 GGA GGA GTG CAG TTT GCC TAT CGT CAC TGT AAT AAC CCT GCT CCC AGA 1920
 Gly Gly Val Gln Phe Ala Tyr Arg His Cys Asn Asn Pro Ala Pro Arg
 AAC AAC GGA CGC TAC TGC ACA GGG AAG AGG GCC ATC TAC CGC TCC TG 1968C
 Asn Asn Gly Arg Tyr Cys Thr Gly Lys Arg Ala Ile Tyr Arg Ser Cys
 AGT CTC ATG CCC TGC CCA CCC AAT GGT AAA TCA TTT CGT CAT GAA CAG 2016
 Ser Leu Met Pro Cys Pro Pro Asn Gly Lys Ser Phe Arg His Glu Gln
 TGT GAG GCC AAA AAT GGC TAT CAG TCT GAT GCA AAA GGA GTC AAA ACT 2064
 Cys Glu Ala Lys Asn Gly Tyr Gln Ser Asp Ala Lys Gly Val Lys Thr
 TTT GTG GAA TGG GTT CCC AAA TAT GCA GGT GTC CTG CCA GCG GAT GTG 2112
 Phe Val Glu Trp Val Pro Lys Tyr Ala Gly Val Leu Pro Ala Asp Val
 TGC AAG CTG ACC TGC AGA GCC AAG GGC ACT GGC TAC TAT GTG GTA TTT 2160
 Cys Lys Leu Thr Cys Arg Ala Lys Gly Thr Gly Tyr Tyr Val Val Phe
 TCT CCA AAG GTG ACC GAT GGC ACT GAA TGT AGG CCG TAC AGT AAT TCC 2208
 Ser Pro Lys Val Thr Asp Gly Thr Glu Cys Arg Pro Tyr Ser Asn Ser
 GTC TGC GTC CGG GGG AAG TGT GTG AGA ACT GGC TGT GAC GGC ATC ATT 2209
 Val Cys Val Arg Gly Lys Cys Val Arg Thr Gly Cys Asp Gly Ile Ile
 GGC TCA AAG CTG CAG TAT GAC AAG TGC GGA GTA TGT GGA GGA GAC AAC 2304
 Gly Ser Lys Leu Gln Tyr Asp Lys Cys Gly Val Cys Gly Gly Asp Asn
 TCC AGC TGT ACA AAG ATT GTT GGA ACC TTT AAT AAG AAA AGT AAG GGT 2352
 Ser Ser Cys Thr Lys Ile Val Gly Thr Phe Asn Lys Lys Ser Lys Gly
 TAC ACT GAC GTG GTG AGG ATT CCT GAA GGG GCA ACC CAC ATA AAA GTT 2400
 Tyr Thr Asp Val Val Arg Ile Pro Glu Gly Ala Thr His Ile Lys Val
 CGA CAG TTC AAA GCC AAA GAC CAG ACT AGA TTC ACT GCC TAT TTA GCC 2448
 Arg Gln Phe Lys Ala Lys Asp Gln Thr Arg Phe Thr Ala Tyr Leu Ala
 CTG AAA AAG AAA AAC GGT GAG TAC CTT ATC AAT GGA AAG TAC ATG ATC 2496
 Leu Lys Lys Lys Asn Gly Glu Tyr Leu Ile Asn Gly Lys Tyr Met Ile
 TCC ACT TCA GAG ACT ATC ATT GAC ATC AAT GGA ACA GTC ATG AAC TAT 2544
 Ser Thr Ser Glu Thr Ile Ile Asp Ile Asn Gly Thr Val Met Asn Tyr
 AGC GGT TGG AGC CAC AGG GAT GAC TTC CTG CAT GGC ATG GGC TAC TCT 2592
 Ser Gly Trp Ser His Arg Asp Asp Phe Leu His Gly Met Gly Tyr Ser
 GCC ACG AAG GAA ATT CTA ATA GTG CAG ATT CTT GCA ACA GAC CCC ACT 2640
 Ala Thr Lys Glu Ile Leu Ile Val Gln Ile Leu Ala Thr Asp Pro Thr
 AAA CCA TTA GAT GTC CGT TAT AGC TTT TTT GTT CCC AAG AAG TCC ACT 2688
 Lys Pro Leu Asp Val Arg Tyr Ser Phe Phe Val Pro Lys Lys Ser Thr
 CCA AAA GTA AAC TCT GTC ACT AGT CAT GGC AGC AAT AAA GTG GGA TCA 2736
 Pro Lys Val Asn Ser Val Thr Ser His Gly Ser Asn Lys Val Gly Ser
 CAC ACT TCG CAG CCG CAG TGG GTC ACG GGC CCA TGG CTC GCC TGC TCT 2784

His Thr Ser Gln Pro Gln Trp Val Thr Gly Pro Trp Leu Ala Cys Ser
 AGG ACC TGT GAC ACA GGT TGG CAC ACC AGA ACG GTG CAG TGC CAG GAT 2832
 Arg Thr Cys Asp Thr Gly Trp His Thr Arg Thr Val Gln Cys Gln Asp
 GGA AAC CGG AAG TTA GCA AAA GGA TGT CCT CTC TCC CAA AGG CCT TCT 2880
 Gly Asn Arg Lys Leu Ala Lys Gly Cys Pro Leu Ser Gln Arg Pro Ser
 GCG TTT AAG CAA TGC TTG TTG AAG AAA TGT TAG CCT GTG GTT ATG ATC 2928
 Ala Phe Lys Gln Cys Leu Leu Lys Lys Cys
 TTA TGC ACA AAG ATA ACT GGA GGA TTC AGC ACC GAT GCA GTC GTG GTG 2976
 AAC AGG AGG TCT ACC TAA CGC ACA GAA AGT CAT GCT TCA GTG ACA TTG 3024
 TCA ACA GGA GTC CAA TTA TGG GCA GAA TCT GCT CTC TGT GAC CAA AAG 3072
 AGG ATG TGC ACT GCT TCA CGT GAC AGT GGT GAC CTT GCA ATA TAG AAA 3120
 AAC TTG GGA GTT ATT GAA CAT CCC CTG GGA TTA CAA GAA ACA CTG ATG 3168
 AAT GTT AAA TCA GGG GAC ATT TGA AGA TGG CAG AAC TGT CTC CCC CTT 3216
 GTC ACC TAC CTC TGA ATA GAA TGT CTT TAA TGG T 3250

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS

(A) LENGTH: 930 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Leu Leu Gly Trp Ala Ser Leu Leu Leu Cys Ala Phe Arg Leu Pro 16
 Leu Ala Ala Val Gly Pro Ala Ala Thr Pro Ala Gln Asp Lys Ala Gly 32
 Gln Pro Pro Thr Ala Ala Ala Ala Ala Gln Pro Arg Arg Arg Gln Gly 48
 Glu Glu Val Gln Glu Arg Ala Glu Pro Pro Gly His Pro His Pro Leu 64
 Ala Gln Arg Arg Arg Ser Lys Gly Leu Val Gln Asn Ile Asp Gln Leu 80
 Tyr Ser Gly Gly Gly Lys Val Gly Tyr Leu Val Tyr Ala Gly Gly Arg 96
 Arg Phe Leu Leu Asp Leu Glu Arg Asp Gly Ser Val Gly Ile Ala Gly 112
 Phe Val Pro Ala Gly Gly Gly Thr Ser Ala Pro Trp Arg His Arg Ser 128
 His Cys Phe Tyr Arg Gly Thr Val Asp Ala Ser Pro Arg Ser Leu Ala 144
 Val Phe Asp Leu Cys Gly Gly Leu Asp Gly Phe Phe Ala Val Lys His 160
 Ala Arg Tyr Thr Leu Lys Pro Leu Leu Arg Gly Pro Trp Ala Glu Glu 176
 Glu Lys Gly Arg Val Tyr Gly Asp Gly Ser Ala Arg Ile Leu His Val 192
 Tyr Thr Arg Glu Gly Phe Ser Phe Glu Ala Leu Pro Pro Arg Ala Ser 208
 Cys Glu Thr Pro Ala Ser Thr Pro Glu Ala His Glu His Ala Pro Ala 224

His Ser Asn Pro Ser Gly Arg Ala Ala Leu Ala Ser Gln Leu Leu Asp 240
 Gln Ser Ala Leu Ser Pro Ala Gly Gly Ser Gly Pro Gln Thr Trp Trp 256
 Arg Arg Arg Arg Arg Ser Ile Ser Arg Ala Arg Gln Val Glu Leu Leu 272
 Leu Val Ala Asp Ala Ser Met Ala Arg Leu Tyr Gly Arg Gly Leu Gln 288
 His Tyr Leu Leu Thr Leu Ala Ser Ile Ala Asn Arg Leu Tyr Ser His 304
 Ala Ser Ile Glu Asn His Ile Arg Leu Ala Val Val Lys Val Val Val 320
 Leu Gly Asp Lys Asp Lys Ser Leu Glu Val Ser Lys Asn Ala Ala Thr 336
 Thr Leu Lys Asn Phe Cys Lys Trp Gln His Gln His Asn Gln Leu Gly 352
 Asp Asp His Glu Glu His Tyr Asp Ala Ala Ile Leu Phe Thr Arg Glu 368
 Asp Leu Cys Gly His His Ser Cys Asp Thr Leu Gly Met Ala Asp Val 384
 Gly Thr Ile Cys Ser Pro Glu Arg Ser Cys Ala Val Ile Glu Asp Asp 400
 Gly Leu His Ala Ala Phe Thr Val Ala His Glu Ile Gly His Leu Leu 416
 Gly Leu Ser His Asp Asp Ser Lys Phe Cys Glu Glu Thr Phe Gly Ser 432
 Thr Glu Asp Lys Arg Leu Met Ser Ser Ile Leu Thr Ser Ile Asp Ala 448
 Ser Lys Pro Trp Ser Lys Cys Thr Ser Ala Thr Ile Thr Glu Phe Leu 464
 Asp Asp Gly His Gly Asn Cys Leu Leu Asp Leu Pro Arg Lys Gln Ile 480
 Leu Gly Pro Glu Glu Leu Pro Gly Gln Thr Tyr Asp Ala Thr Gln Gln 496
 Cys Asn Leu Thr Phe Gly Pro Glu Tyr Ser Val Cys Pro Gly Met Asp 512
 Val Cys Ala Arg Leu Trp Cys Ala Val Val Arg Gln Gly Gln Met Val 528
 Cys Leu Thr Lys Lys Leu Pro Ala Val Glu Gly Thr Pro Cys Gly Lys 544
 Gly Arg Ile Cys Leu Gln Gly Lys Cys Val Asp Lys Thr Lys Lys Lys 560
 Tyr Tyr Ser Thr Ser Ser His Gly Asn Trp Gly Ser Trp Gly Ser Trp 576
 Gly Gln Cys Ser Arg Ser Cys Gly Gly Gly Val Gln Phe Ala Tyr Arg 592
 His Cys Asn Asn Pro Ala Pro Arg Asn Asn Gly Arg Tyr Cys Thr Gly 608
 Lys Arg Ala Ile Tyr Arg Ser Cys Ser Leu Met Pro Cys Pro Pro Asn 624
 Gly Lys Ser Phe Arg His Glu Gln Cys Glu Ala Lys Asn Gly Tyr Gln 640
 Ser Asp Ala Lys Gly Val Lys Thr Phe Val Glu Trp Val Pro Lys Tyr 656
 Ala Gly Val Leu Pro Ala Asp Val Cys Lys Leu Thr Cys Arg Ala Lys 672
 Gly Thr Gly Tyr Tyr Val Val Phe Ser Pro Lys Val Thr Asp Gly Thr 688
 Glu Cys Arg Pro Tyr Ser Asn Ser Val Cys Val Arg Gly Lys Cys Val 704
 Arg Thr Gly Cys Asp Gly Ile Ile Gly Ser Lys Leu Gln Tyr Asp Lys 720
 Cys Gly Val Cys Gly Gly Asp Asn Ser Ser Cys Thr Lys Ile Val Gly 736

Thr Phe Asn Lys Lys Ser Lys Gly Tyr Thr Asp Val Val Arg Ile Pro	752
Glu Gly Ala Thr His Ile Lys Val Arg Gln Phe Lys Ala Lys Asp Gln	768
Thr Arg Phe Thr Ala Tyr Leu Ala Leu Lys Lys Lys Asn Gly Glu Tyr	784
Leu Ile Asn Gly Lys Tyr Met Ile Ser Thr Ser Glu Thr Ile Ile Asp	800
Ile Asn Gly Thr Val Met Asn Tyr Ser Gly Trp Ser His Arg Asp Asp	816
Phe Leu His Gly Met Gly Tyr Ser Ala Thr Lys Glu Ile Leu Ile Val	832
Gln Ile Leu Ala Thr Asp Pro Thr Lys Pro Leu Asp Val Arg Tyr Ser	848
Phe Phe Val Pro Lys Lys Ser Thr Pro Lys Val Asn Ser Val Thr Ser	864
His Gly Ser Asn Lys Val Gly Ser His Thr Ser Gln Pro Gln Trp Val	880
Thr Gly Pro Trp Leu Ala Cys Ser Arg Thr Cys Asp Thr Gly Trp His	896
Thr Arg Thr Val Gln Cys Gln Asp Gly Asn Arg Lys Leu Ala Lys Gly	912
Cys Pro Leu Ser Gln Arg Pro Ser Ala Phe Lys Gln Cys Leu Leu Lys	928
Lys Cys	930

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS
 - (A) LENGTH: 42 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

SISRARQVELLLVADASMARMYGRGLQHLLTLASIANKLYF

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

CGGCCACGACCCTCAAGAACTTT

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

GCATGGAGGCCATCATCTTCAATCA

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GGGAGGATTTATGTGGGCATCA

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GTGCATTTGGACCAGGGCTTAGA

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

SISRARQVELLAhxC-amide